



OIPE

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/896,522

DATE: 01/26/2002

TIME: 16:07:13

Input Set : N:\jumbos\896522.txt

Output Set: N:\CRF3\01252002\I896522.raw

```

3 <110> APPLICANT: Glucksmann, Maria A.
5 <120> TITLE OF INVENTION: 57658, A NOVEL HUMAN URIDINE KINASE AND
6   USES THEREOF
8 <130> FILE REFERENCE: 381552001700
10 <140> CURRENT APPLICATION NUMBER: 09/896,522
11 <141> CURRENT FILING DATE: 2001-06-28
13 <150> PRIOR APPLICATION NUMBER: 60/216,503
14 <151> PRIOR FILING DATE: 2000-06-30
16 <160> NUMBER OF SEQ ID NOS: 6
18 <170> SOFTWARE: FastSEQ for Windows Version 4.0
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 1624
22 <212> TYPE: DNA
23 <213> ORGANISM: Homo sapiens
25 <220> FEATURE:
26 <221> NAME/KEY: CDS
27 <222> LOCATION: (94)...(927)
29 <400> SEQUENCE: 1
30 gtgggggtcgc ctccgacctc ggcgctgggc gggcgcgccg ggcccgggga aggggcgggc      60
31 gcggggaccc gatgcgcggg agcggaggcc gag atg gct tcg gcg gga ggc gaa      114
32                                     Met Ala Ser Ala Gly Gly Glu
33                                     1               5
35 gac tgc gag agc ccc gcg ccg gag gcc gac cgt ccg cac cag cgg ccc      162
36 Asp Cys Glu Ser Pro Ala Pro Glu Ala Asp Arg Pro His Gln Arg Pro
37      10               15               20
39 ttc ctg ata ggg gtg agc ggc gcc act gcc agc ggg aag tcg acc gtg      210
40 Phe Leu Ile Gly Val Ser Gly Gly Thr Ala Ser Gly Lys Ser Thr Val
41      25               30               35
43 tgt gag aag atc atg gag ttg ctg gga cag aac gag gtg gaa cag cgg      258
44 Cys Glu Lys Ile Met Glu Leu Leu Gly Gln Asn Glu Val Glu Gln Arg
45 40               45               50               55
47 cag cgg aag gtg gtc atc ctg agc cag gac agg ttc tac aag gtc ctg      306
48 Gln Arg Lys Val Val Ile Leu Ser Gln Asp Arg Phe Tyr Lys Val Leu
49      60               65               70
51 acg gca gag cag aag gcc aag gcc ttg aaa gga cag tac aat ttt gac      354
52 Thr Ala Glu Gln Lys Ala Lys Ala Leu Lys Gly Gln Tyr Asn Phe Asp
53      75               80               85
55 cat cca gat gcc ttt gat aat gat ttg atg cac agg act ctg aag aac      402
56 His Pro Asp Ala Phe Asp Asn Asp Leu Met His Arg Thr Leu Lys Asn
57      90               95               100
59 atc gtg gag ggc aaa acg gtg gag gtg ccg acc tat gat ttt gtg aca      450
60 Ile Val Glu Gly Lys Thr Val Glu Val Pro Thr Tyr Asp Phe Val Thr
61      105               110               115

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```

63 cac tca agg tta cca gag acc acg gtg gtc tac cct gcg gac gtg gtt      498
64 His Ser Arg Leu Pro Glu Thr Thr Val Val Tyr Pro Ala Asp Val Val
65 120                               125                               130                               135
67 ctg ttt gag ggc atc ttg gtg ttc tac agc cag gag atc cgg gac atg      546
68 Leu Phe Glu Gly Ile Leu Val Phe Tyr Ser Gln Glu Ile Arg Asp Met
69                               140                               145                               150
71 ttc cac ctg cgc ctc ttc gtg gac acc gac tcc gac gtc agg ctg tct      594
72 Phe His Leu Arg Leu Phe Val Asp Thr Asp Ser Asp Val Arg Leu Ser
73                               155                               160                               165
75 cga aga gtt ctc cgg gac gtg cgc cga ggg agg gac ctg gag cag att      642
76 Arg Arg Val Leu Arg Asp Val Arg Arg Gly Arg Asp Leu Glu Gln Ile
77                               170                               175                               180
79 ctg acg cag tac acc acc ttc gtg aag ccg gcc ttc gag gag ttc tgc      690
80 Leu Thr Gln Tyr Thr Thr Phe Val Lys Pro Ala Phe Glu Glu Phe Cys
81                               185                               190                               195
83 ctg ccg aca aag aag tat gcc gat gtg atc atc cca cga gga gtg gac      738
84 Leu Pro Thr Lys Lys Tyr Ala Asp Val Ile Ile Pro Arg Gly Val Asp
85 200                               205                               210                               215
87 aat atg gtt gcc atc aac ctg atc gtg cag cac atc cag gac att ctg      786
88 Asn Met Val Ala Ile Asn Leu Ile Val Gln His Ile Gln Asp Ile Leu
89                               220                               225                               230
91 aat ggt gac atc tgc aaa tgg cac cga gga ggg tcc aat ggg cgg agc      834
92 Asn Gly Asp Ile Cys Lys Trp His Arg Gly Gly Ser Asn Gly Arg Ser
93                               235                               240                               245
95 tac aag cgg acc ttt tct gag cca ggg gac cac cct ggg atg ctg acc      882
96 Tyr Lys Arg Thr Phe Ser Glu Pro Gly Asp His Pro Gly Met Leu Thr
97                               250                               255                               260
99 tct ggc aaa cgg tca cat ttg gag tcc agc agc aga ccc cac tga      927
100 Ser Gly Lys Arg Ser His Leu Glu Ser Ser Ser Arg Pro His *
101                               265                               270                               275
103 ggggctgccg agcctcaggg caggctctccc gcccggcacg tgtgttcagg gactgagcct      987
104 ggggacgccc acccacaccc actgcttcct ctcggcgcac cccaggggag tgtagcagc      1047
105 gaggccttcc tcaactcagga gtggaaactc agatgtgtca ctcagactca acttgctggg      1107
106 aactgacag gcgttcctga ggttttcagc cacttaggct cgttgcggtt taaagatccc      1167
107 tctaggtcac tgagaaatgc cacagaatgt gcaggaagcc tgggaggctt ctgtgaggaa      1227
108 tgtgaggcac attattgggg aaattgagga gacagcctag aactggctg gcctgatgtt      1287
109 ttgttgacag tgaaccaca gtgggagaga gttttttcca gtctgatctg gttcttacac      1347
110 actcacacac ataactcaaa agttttgtga acaagtactt tcctttttta catgttacat      1407
111 gtcctcatgt tttctgtttt ctgtttcata acacaaggct ggttgtggcc tacaaccta      1467
112 atttcatgac ccagtgtttt gcagtcagc gtggcctaca cggatatggg gagccactga      1527
113 gggatgtttt ccccttgc ttgtgcctta aaggcagaga agcgaggcgg atgccctgga      1587
114 agcaccagc atcacacca ggcttgtgcg gggccag      1624
116 <210> SEQ ID NO: 2
117 <211> LENGTH: 277
118 <212> TYPE: PRT
119 <213> ORGANISM: Homo sapiens
121 <400> SEQUENCE: 2
122 Met Ala Ser Ala Gly Gly Glu Asp Cys Glu Ser Pro Ala Pro Glu Ala
123 1                               5                               10                               15

```

## RAW SEQUENCE LISTING

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Input Set : N:\jumbos\896522.txt

Output Set: N:\CRF3\01252002\I896522.raw

```
124 Asp Arg Pro His Gln Arg Pro Phe Leu Ile Gly Val Ser Gly Gly Thr
125          20          25          30
126 Ala Ser Gly Lys Ser Thr Val Cys Glu Lys Ile Met Glu Leu Leu Gly
127          35          40          45
128 Gln Asn Glu Val Glu Gln Arg Gln Arg Lys Val Val Ile Leu Ser Gln
129          50          55          60
130 Asp Arg Phe Tyr Lys Val Leu Thr Ala Glu Gln Lys Ala Lys Ala Leu
131 65          70          75          80
132 Lys Gly Gln Tyr Asn Phe Asp His Pro Asp Ala Phe Asp Asn Asp Leu
133          85          90          95
134 Met His Arg Thr Leu Lys Asn Ile Val Glu Gly Lys Thr Val Glu Val
135          100         105         110
136 Pro Thr Tyr Asp Phe Val Thr His Ser Arg Leu Pro Glu Thr Thr Val
137          115         120         125
138 Val Tyr Pro Ala Asp Val Val Leu Phe Glu Gly Ile Leu Val Phe Tyr
139          130         135         140
140 Ser Gln Glu Ile Arg Asp Met Phe His Leu Arg Leu Phe Val Asp Thr
141 145         150         155         160
142 Asp Ser Asp Val Arg Leu Ser Arg Arg Val Leu Arg Asp Val Arg Arg
143          165         170         175
144 Gly Arg Asp Leu Glu Gln Ile Leu Thr Gln Tyr Thr Thr Phe Val Lys
145          180         185         190
146 Pro Ala Phe Glu Glu Phe Cys Leu Pro Thr Lys Lys Tyr Ala Asp Val
147          195         200         205
148 Ile Ile Pro Arg Gly Val Asp Asn Met Val Ala Ile Asn Leu Ile Val
149          210         215         220
150 Gln His Ile Gln Asp Ile Leu Asn Gly Asp Ile Cys Lys Trp His Arg
151 225         230         235         240
152 Gly Gly Ser Asn Gly Arg Ser Tyr Lys Arg Thr Phe Ser Glu Pro Gly
153          245         250         255
154 Asp His Pro Gly Met Leu Thr Ser Gly Lys Arg Ser His Leu Glu Ser
155          260         265         270
156 Ser Ser Arg Pro His
157          275
159 <210> SEQ ID NO: 3
160 <211> LENGTH: 834
161 <212> TYPE: DNA
162 <213> ORGANISM: Homo sapiens
164 <400> SEQUENCE: 3
165 atggtcttcgg cgggaggcga agactgcgag agccccgcgc cggaggccga ccgtccgcac      60
166 cagcggccct tctgatagg ggtgagcggc ggcactgcc a gcggaagtc gaccgtgtgt      120
167 gagaagatca tggagttgct gggacagaac gaggtggaac agcggcagcg gaaggtggtc      180
168 atcctgagcc aggacaggtt ctacaaggct ctgacggcag agcagaaggc caaggccttg      240
169 aaaggacagt acaattttga ccatccagat gcctttgata atgatttgat gcacaggact      300
170 ctgaagaaca tcgtggaggg caaaacgggtg gaggtgccga cctatgattt tgtgacacac      360
171 tcaaggttac cagagaccac ggtggtctac cctgcggacg tggttctgtt tgagggcatc      420
172 ttggtgttct acagccagga gatccgggac atgttccacc tgcgcctctt cgtggacacc      480
173 gactccgacg tcaggctgtc tcgaagagtt ctccgggacg tgcgccgagg gagggacctg      540
174 gacgagattc tgacgcagta caccaccttc gtgaagccgg ccttcgagga gttctgcctg      600
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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/896,522

DATE: 01/26/2002

TIME: 16:07:13

Input Set : N:\jumbos\896522.txt

Output Set: N:\CRF3\01252002\I896522.raw

```

175 ccgacaaaga agtatgccga tgtgatcatc ccacgaggag tggacaatat ggttgccatc      660
176 aacctgatcg tgcagcacat ccaggacatt ctgaatgggtg acatctgcaa atggcaccga      720
177 ggaggggtcca atgggaggag ctacaagcgg accttttctg agccagggga ccaccctggg      780
178 atgctgacct ctggcaaacg gtcacatttg gagtccagca gcagaccca ctga      834
180 <210> SEQ ID NO: 4
181 <211> LENGTH: 231
182 <212> TYPE: PRT
183 <213> ORGANISM: Artificial Sequence
185 <220> FEATURE:
186 <223> OTHER INFORMATION: Consensus amino acid sequence
188 <400> SEQUENCE: 4
189 Val Ile Gly Val Ala Gly Ser Ser Gly Ala Gly Lys Thr Thr Val Ala
190 1 5 10 15
191 Arg Arg Ile Val Ser Ile Phe Gly Arg Glu Gly Val Pro Ala Ala Gly
192 20 25 30
193 Ile Glu Gly Asn Pro Asp Ser Asn Thr Gly Asp Ser Phe Leu Arg Leu
194 35 40 45
195 Asp Arg Phe Tyr Met Asp Leu His Leu Glu Asp Arg Lys Arg Ala Gly
196 50 55 60
197 Asn Lys His Tyr Ser Phe Phe Ser Pro Glu Ala Asn Asp Phe Asp Leu
198 65 70 75 80
199 Leu Tyr Glu Val Phe Lys Glu Leu Lys Glu Gly Lys Ser Val Asp Lys
200 85 90 95
201 Pro Ile Tyr Asn His Val Thr Gly Glu Arg Asp Pro Asp Gly Gln Glu
202 100 105 110
203 Pro Gly Thr Phe Thr Asp Trp Pro Glu Leu Ile Glu Gly Ala Asp Val
204 115 120 125
205 Leu Val Ile Glu Gly Leu His Ala Leu Tyr Asp Glu Arg Glu Val Asn
206 130 135 140
207 Val Ala Gln Leu Leu Asp Leu Lys Ile Tyr Val Asp Pro Asp Ile Asp
208 145 150 155 160
209 Leu Glu Leu Ala Arg Lys Ile Gln Arg Asp Met Ala Glu Arg Gly His
210 165 170 175
211 Ser Leu Glu Gly Val Leu Asp Ser Ile Glu Lys Arg Arg Lys Pro Asp
212 180 185 190
213 Tyr Val Asn Tyr Ile Ala Pro Gln Phe Ser Tyr Ala Asp Leu Ile Ile
214 195 200 205
215 Gln Arg Val Pro Thr Val Asp Thr Ser Asn Asp Phe Ile Ala Lys Ile
216 210 215 220
217 Ile Pro Val Arg Asp Glu Leu
218 225 230
220 <210> SEQ ID NO: 5
221 <211> LENGTH: 125
222 <212> TYPE: PRT
223 <213> ORGANISM: Artificial Sequence
225 <220> FEATURE:
226 <223> OTHER INFORMATION: Consensus amino acid sequence
228 <400> SEQUENCE: 5
229 Leu Lys Ile Phe Val Asp Thr Asp Ala Asp Val Arg Leu Ile Arg Arg

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## RAW SEQUENCE LISTING

DATE: 01/26/2002

PATENT APPLICATION: US/09/896,522

TIME: 16:07:13

Input Set : N:\jumbos\896522.txt

Output Set: N:\CRF3\01252002\I896522.raw

```

230 1           5           10           15
231 Ile Lys Arg Asp Val Asn Glu Arg Gly Arg Asp Ile Glu Ser Val Ile
232           20           25           30
233 Glu Gln Tyr Met Lys Phe Val Lys Pro Met Tyr Glu Gln Phe Ile Glu
234           35           40           45
235 Pro Thr Lys Lys Tyr Ala Asp Ile Ile Ile Pro Arg Gly Gly Asp Asn
236           50           55           60
237 His Val Ala Ile Asp Leu Ile Val Gln His Ile Gln Ser Ile Leu Asn
238 65           70           75           80
239 Glu Gly Leu Ser Ser Gln His Thr Asn Tyr Met Val Asn Arg Ser Tyr
240           85           90           95
241 Lys Arg Thr Phe Ser Glu Pro Gly Asp His Pro Gly Tyr Thr Pro Ser
242           100          105          110
243 Gly Lys Arg Gln His Leu Glu Ser Ser Arg Pro His
244           115          120          125
246 <210> SEQ ID NO: 6
247 <211> LENGTH: 124
248 <212> TYPE: PRT
249 <213> ORGANISM: Artificial Sequence
251 <220> FEATURE:
252 <223> OTHER INFORMATION: Consensus amino acid sequence
254 <400> SEQUENCE: 6
255 Ile Ile Gly Ile Ala Gly Gly Ser Gly Ser Gly Lys Thr Thr Ile Ala
256 1           5           10           15
257 Arg Lys Ile Val Glu Met Leu Asn Lys Pro Gly Gln Glu Lys Val Val
258           20           25           30
259 Ile Ile Ser Gln Asp Asn Tyr Tyr Lys Asp Leu Ser Glu Leu Asp Met
260           35           40           45
261 Glu Glu Arg Lys Glu Asn Asn Tyr Asn Phe Asp His Pro Asp Ala Phe
262           50           55           60
263 Asp Phe Asp Leu Leu Tyr Glu His Leu Lys Asx Leu Lys Asn Gly Lys
264 65           70           75           80
265 Ser Val Glu Val Pro Ile Tyr Asp Phe Lys Thr His His Arg Arg Lys
266           85           90           95
267 Asp Glu Thr Val Thr Ile Glu Pro Ala Asp Val Ile Ile Leu Glu Gly
268           100          105          110
269 Ile Tyr Ala Leu Tyr Asp Glu Arg Ile Arg Asp Leu
270           115          120

```

## VERIFICATION SUMMARY

DATE: 01/26/2002

PATENT APPLICATION: US/09/896,522

TIME: 16:07:14

Input Set : N:\jumbos\896522.txt

Output Set: N:\CRF3\01252002\I896522.raw



OIPE

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/896,522

DATE: 01/19/2002

TIME: 11:19:29

Input Set : D:\38155-20017 SEQ Listing.txt  
 Output Set: N:\CRF3\01192002\I896522.raw

**Does Not Comply**  
**Corrected Diskette Needed**

3 <110> APPLICANT: Glucksmann, Maria A.  
 5 <120> TITLE OF INVENTION: 57658, A NOVEL HUMAN URIDINE KINASE AND  
 6 USES THEREOF  
 8 <130> FILE REFERENCE: 381552001700  
 10 <140> CURRENT APPLICATION NUMBER: 09/896,522  
 11 <141> CURRENT FILING DATE: 2001-06-28  
 13 <150> PRIOR APPLICATION NUMBER: 60/216,503  
 14 <151> PRIOR FILING DATE: 2000-06-30  
 16 <160> NUMBER OF SEQ ID NOS: 6  
 18 <170> SOFTWARE: FastSEQ for Windows Version 4.0

## ERRORED SEQUENCES

246 <210> SEQ ID NO: 6  
 247 <211> LENGTH: 124  
 248 <212> TYPE: PRT  
 249 <213> ORGANISM: Artificial Sequence  
 251 <220> FEATURE:  
 252 <223> OTHER INFORMATION: Consensus amino acid sequence  
 254 <400> SEQUENCE: 6  
 255 Ile Ile Gly Ile Ala Gly Gly Ser Gly Ser Gly Lys Thr Thr Ile Ala  
 256 1 5 10 15  
 257 Arg Lys Ile Val Glu Met Leu Asn Lys Pro Gly Gln Glu Lys Val Val  
 258 20 25 30  
 259 Ile Ile Ser Gln Asp Asn Tyr Tyr Lys Asp Leu Ser Glu Leu Asp Met  
 260 35 40 45  
 261 Glu Glu Arg Lys Glu Asn Asn Tyr Asn Phe Asp His Pro Asp Ala Phe  
 262 50 55 60  
 263 Asp Phe Asp Leu Leu Tyr Glu His Leu Lys Asx Leu Lys Asn Gly Lys  
 264 65 70 75 80  
 265 Ser Val Glu Val Pro Ile Tyr Asp Phe Lys Thr His His Arg Arg Lys  
 266 85 90 95  
 267 Asp Glu Thr Val Thr Ile Glu Pro Ala Asp Val Ile Ile Leu Glu Gly  
 268 100 105 110  
 269 Ile Tyr Ala Leu Tyr Asp Glu Arg Ile Arg Asp Leu  
 270 115 120

E--&gt; 272 (1)

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/896,522

DATE: 01/19/2002

TIME: 11:19:30

Input Set : D:\38155-20017 SEQ Listing.txt

Output Set: N:\CRF3\01192002\I896522.raw

L:272 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:6



CRF Errors Corrected by the STIC Systems Branch

Serial Number: 09/896,522

CRF Processing Date: 1/26/2002  
 Edited by: [Signature]  
 Verified by: [Signature] (STIC staff)

**ENTERED**

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: \_\_\_\_\_
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other \_\_\_\_\_
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: \_\_\_\_\_
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: \_\_\_\_\_
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: \_\_\_\_\_
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: \_\_\_\_\_
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: \_\_\_\_\_
- ☒ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file;  
☐ page numbers throughout text; ☐ other invalid text, such as \_\_\_\_\_
- ☐ Inserted mandatory headings, specifically: \_\_\_\_\_
- ☐ Corrected an obvious error in the response, specifically: \_\_\_\_\_
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: \_\_\_\_\_
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted **ending** stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: \_\_\_\_\_
- ☐ Other: \_\_\_\_\_

\*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95